



Names of God



A review of the expression and methylation pattern of *Wif1* and *WT1* genes ,in different types of cancers.

By :
zahra mohammadi

Supervisor :
Dr. Gheibi

□Content:

❖Introduction

✓ Importance of Wnt signaling pathway

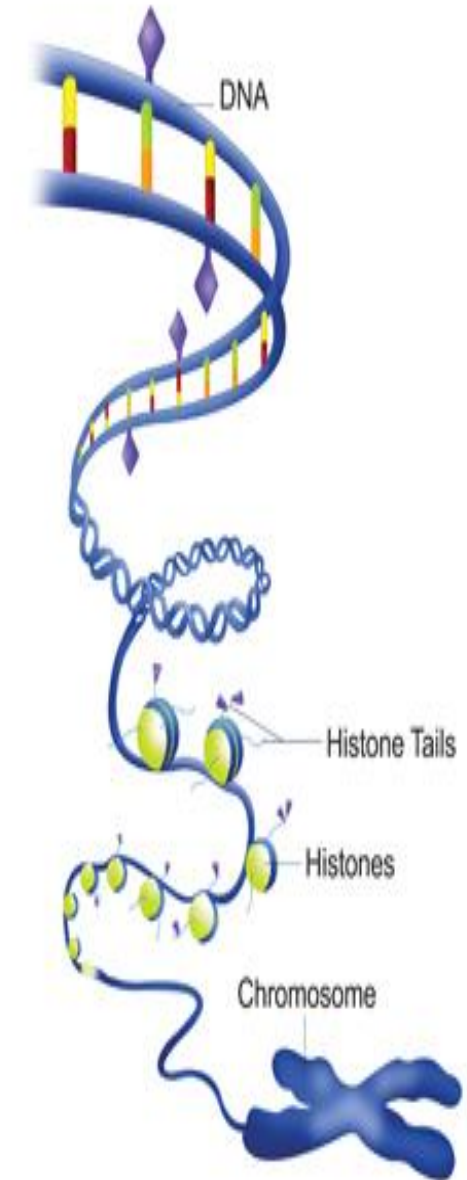
❖ *Wif1*

❖ *WT1*

❖Epigenetic changes

✓ DNA Methylation

❖Literature review



Wnt signaling importance: (1)

- Is an ancient and evolutionarily conserved pathway that regulates crucial aspects of:
 - ✓ Cell fate determination.
 - ✓ Cell migration.
 - ✓ Organogenesis during embryonic development.
 - ✓

Wnt signaling pathways:

Including : (2)

- 1) The canonical or Wnt/ β -catenin dependent pathway
- 2) The non-canonical or β -catenin-independent pathway
which can be divided into the:
 - ✓ Planar Cell Polarity pathway
 - ✓ the Wnt/ Ca^{2+} pathway

Wnt Signaling Pathway

Canonical

B,catenin

Non-canonical

Ca²⁺

PCP

Osteoblast cell proliferation

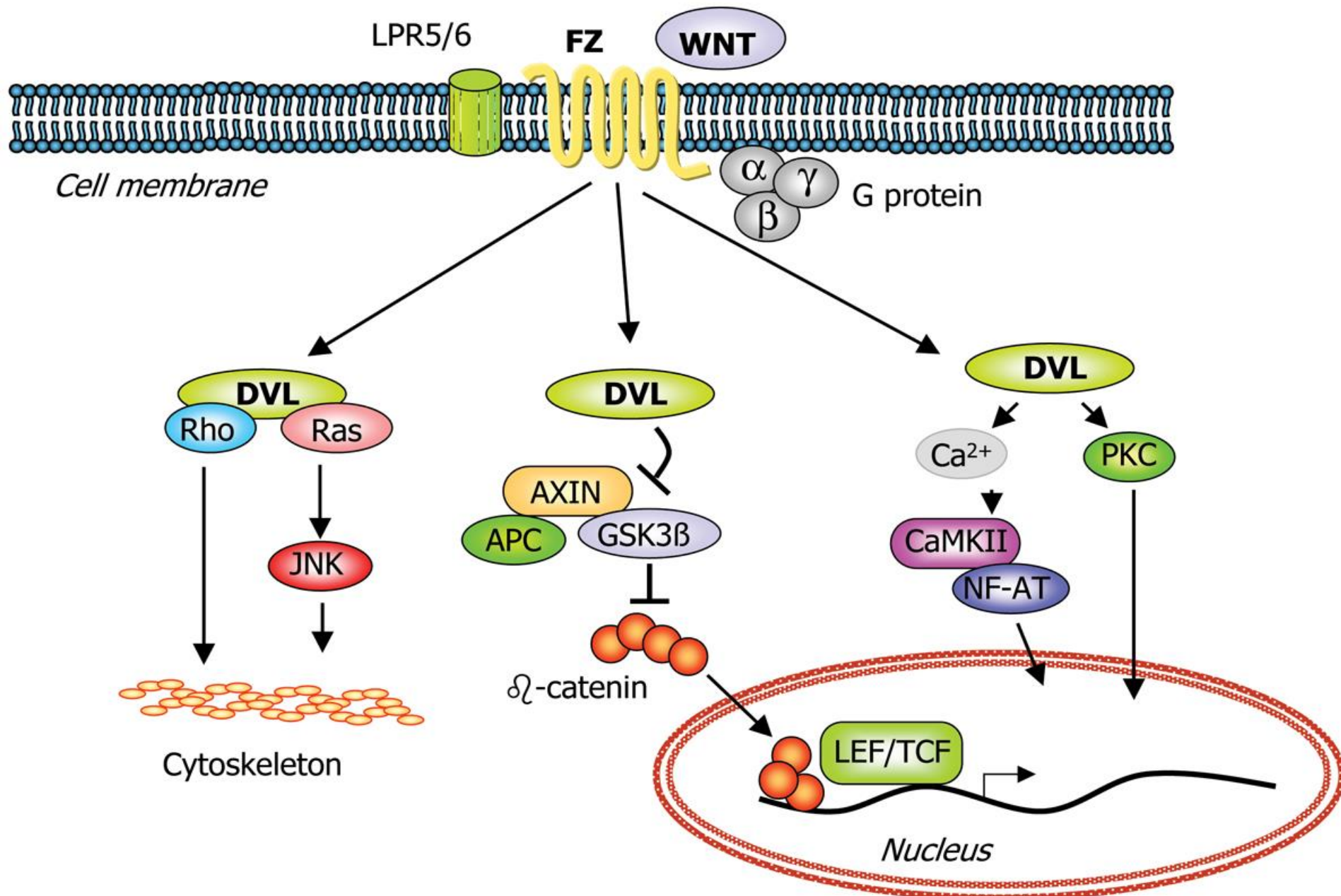
- Cell fate determination
- General bone maintenance
- Body axis specification
- Cancer**

intracellular Ca²⁺
conc.

Activation of JNK

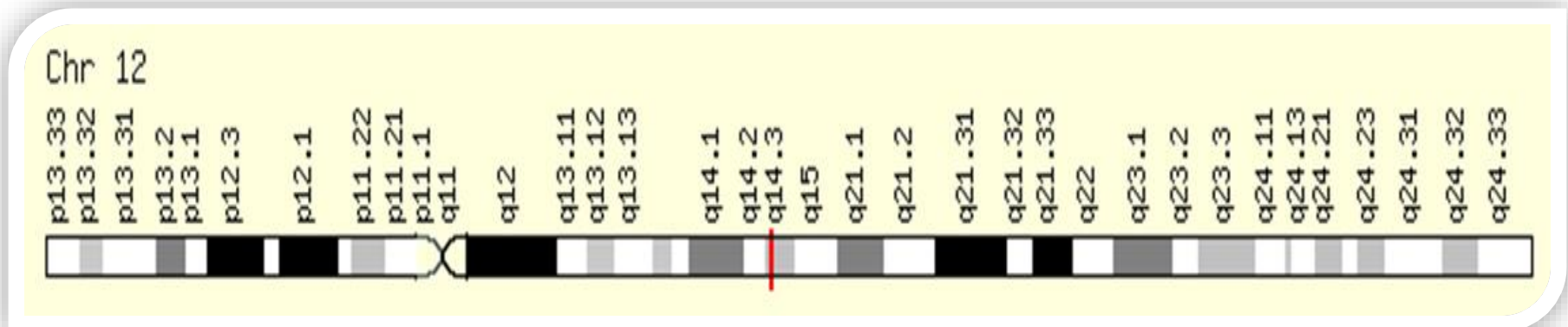
Affect cytoskeletal organisation

WNT signaling



WIF1

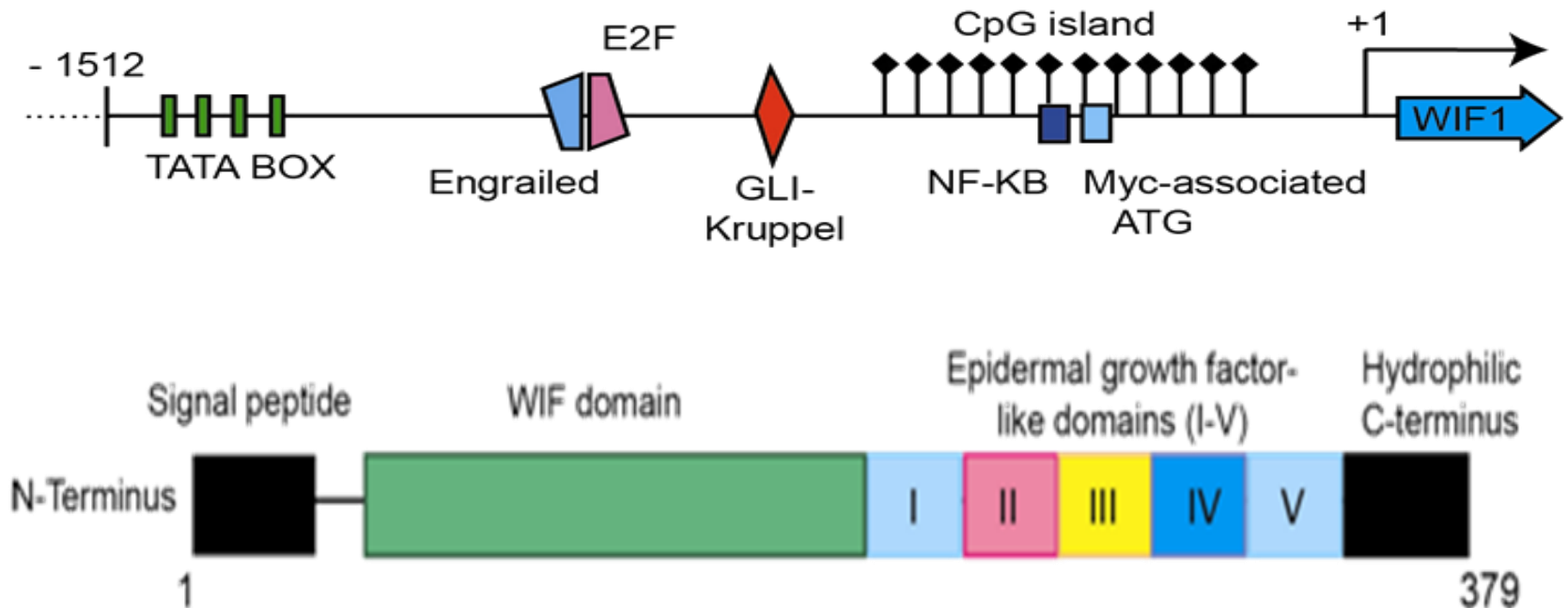
- Wnt inhibitory factor-1 , a secreted protein that binds to Wnt proteins and inhibits their activities. (3)
- WIF1 are potentially important in cancers as **Wnt pathway inhibitors** and **increased apoptosis**. (4)



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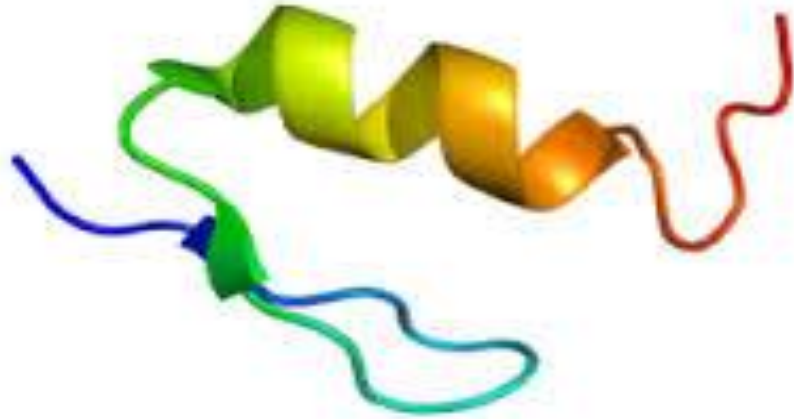
WIF₁

- This protein contains a WNT inhibitory factor (WIF) domain and 5 epidermal growth factor (EGF)-like domains. (5)



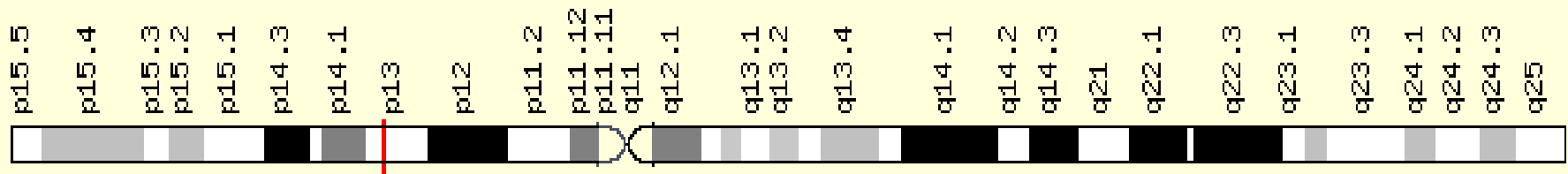
WT1

- 11p13
- 7490 bp



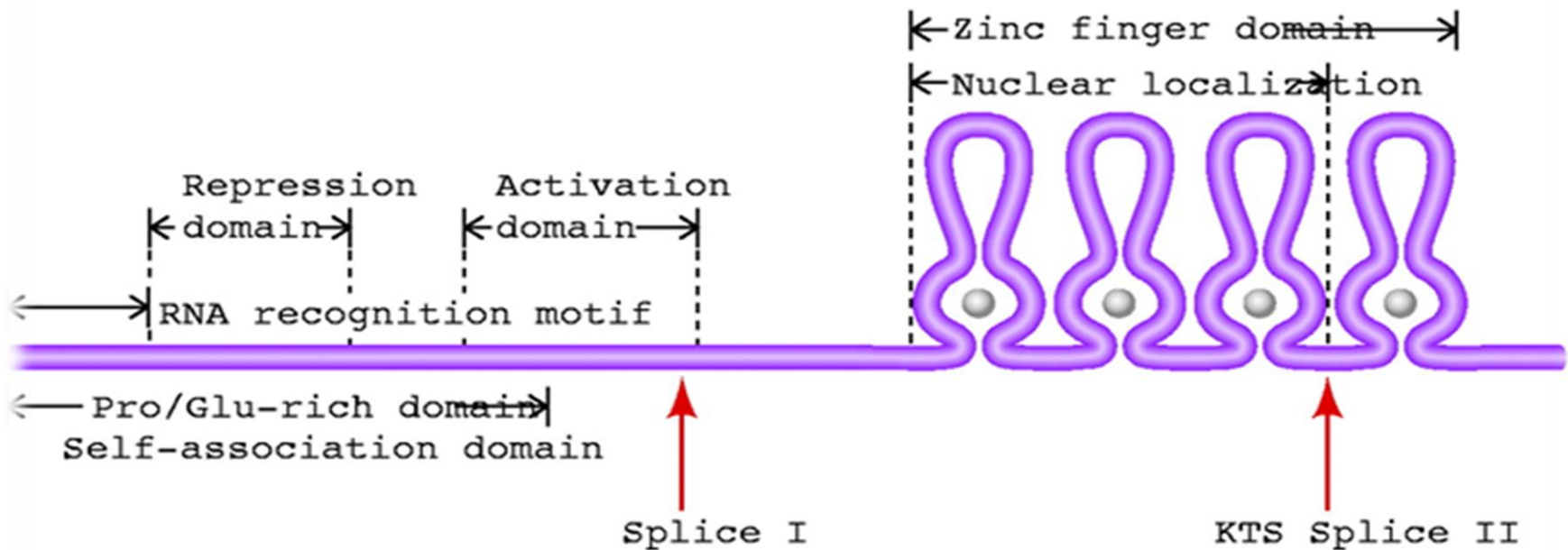
WT1 could be the role of the **tumor suppressor** or **Oncogene**. (6)

Chr 11



- WT1 encodes a zinc-finger transcription factor expressed in kidney, gonads, spleen, and mesothelium. (7)

B Structure of WT1 protein



GENETICS



mutations



inherited

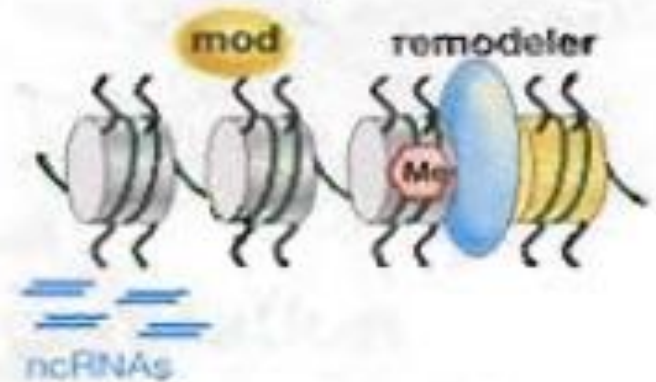
germ line

species

EPIGENETICS



alterations

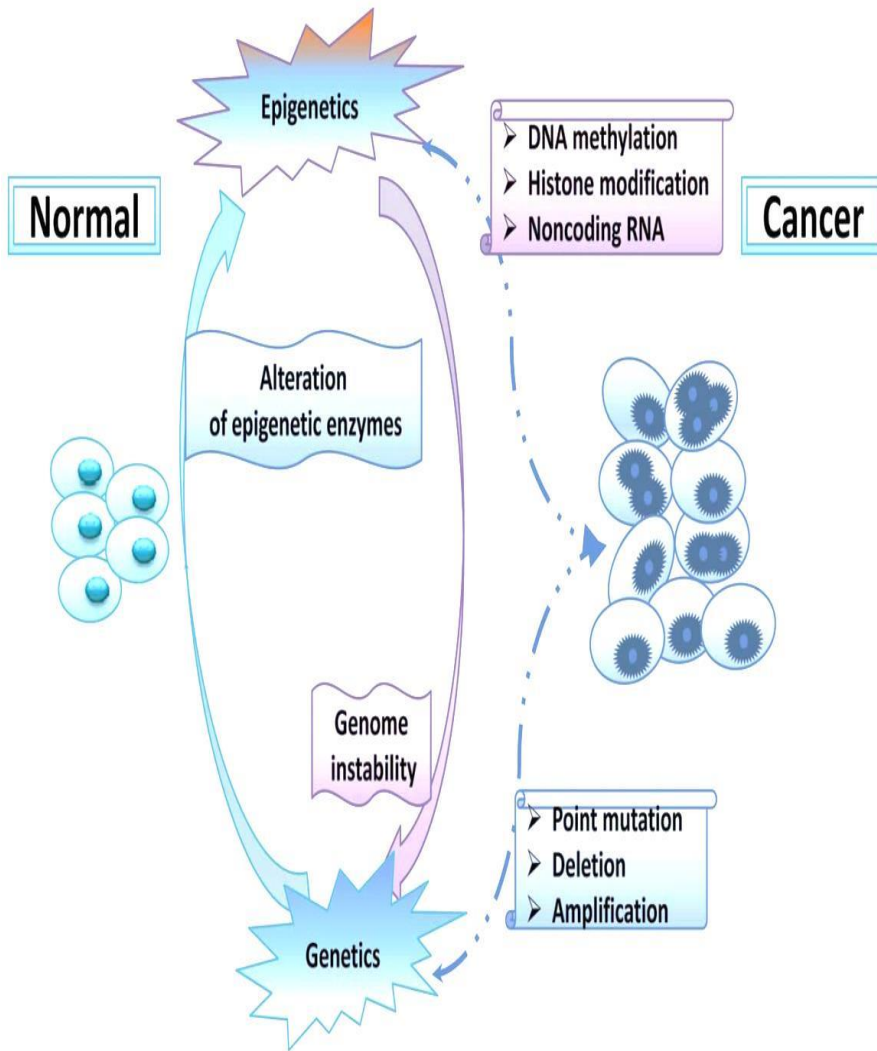


stable?

soma

variability

Defining Epigenetics



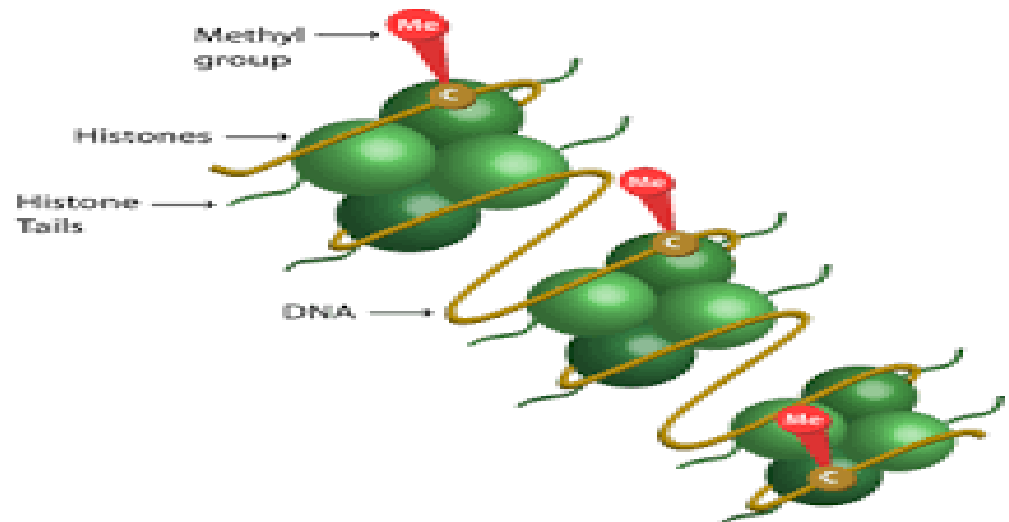
- Reversible changes in gene expression/function **without** changes in DNA sequence.
- Can be inherited from precursor cells. (8)

DNA methylation

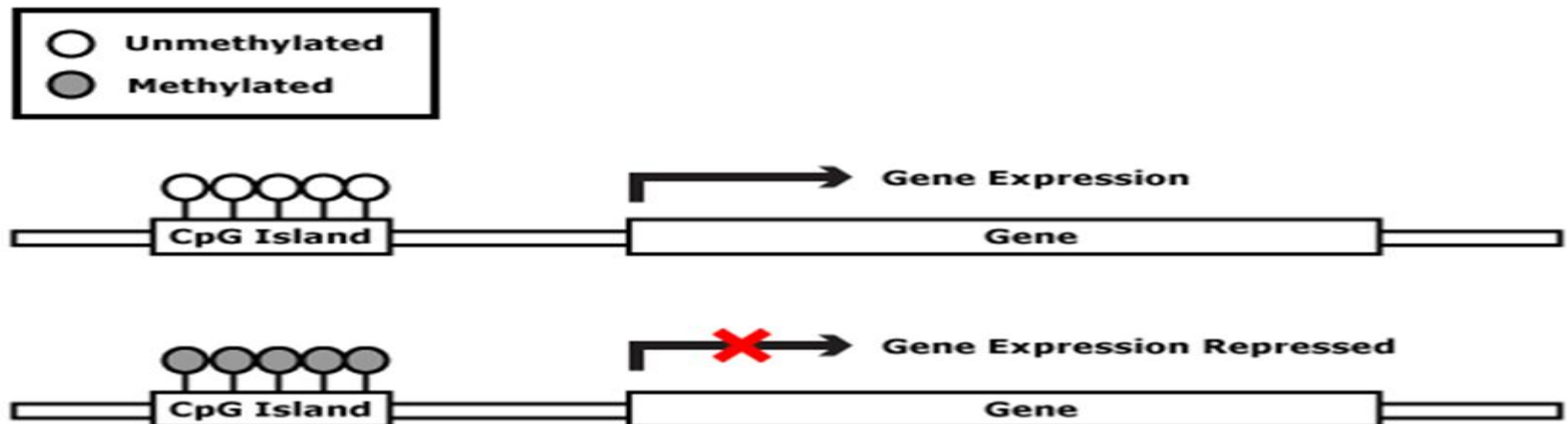
❖ is an epigenetic marks associated with transcriptional regulation and genome structure. (9)

❖ Epigenetic changes in signaling pathway:

Wnt / B.catenin could be an attractive strategy for cancer therapy is dependent on the Wnt. (10)



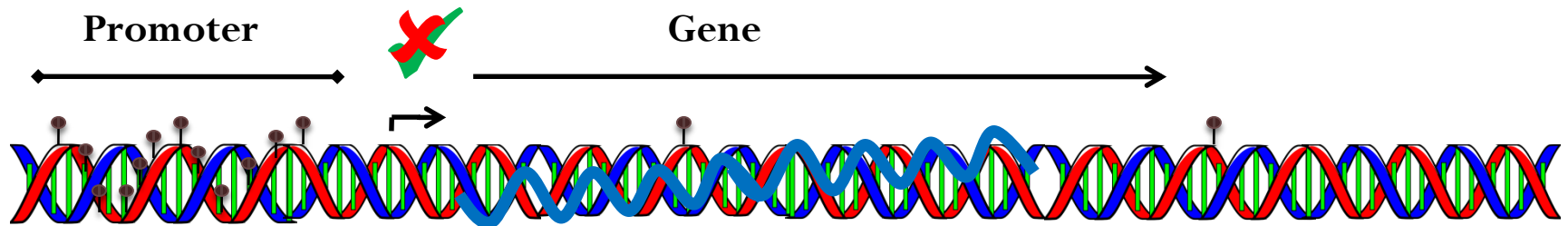
- Methylation considered as a control mechanism of the gene profile while the activity of oncogenes cause development of tumor.
- Tumor suppressor factors play an important role in controlling and changing the genetic profile of terminally differentiated cells. (11)



What does DNA methylation do?

Global Methylation

Regional Methylation

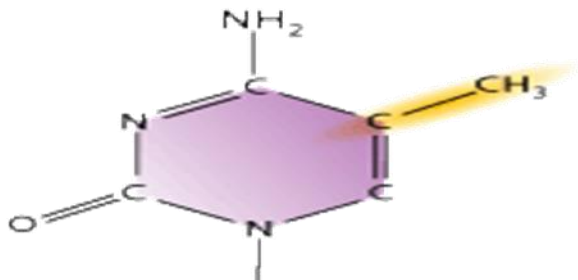
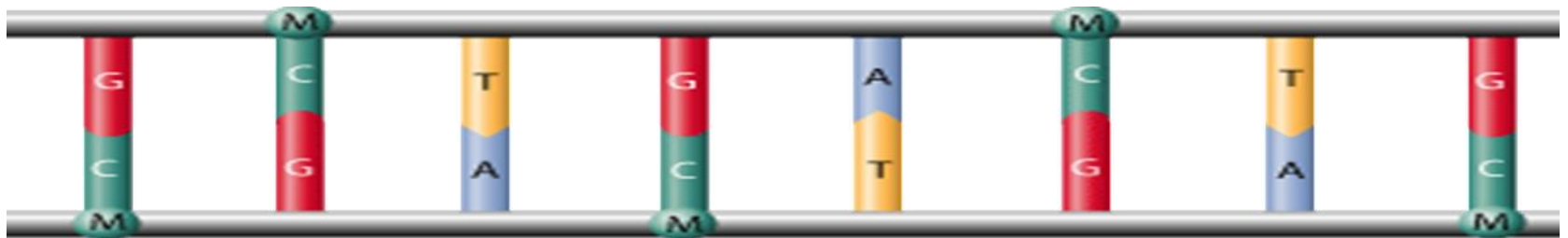


- ❖ High Density – CpG Islands (CGIs)
- ❖ Located in promoters and introns
- ❖ Gene Silencing

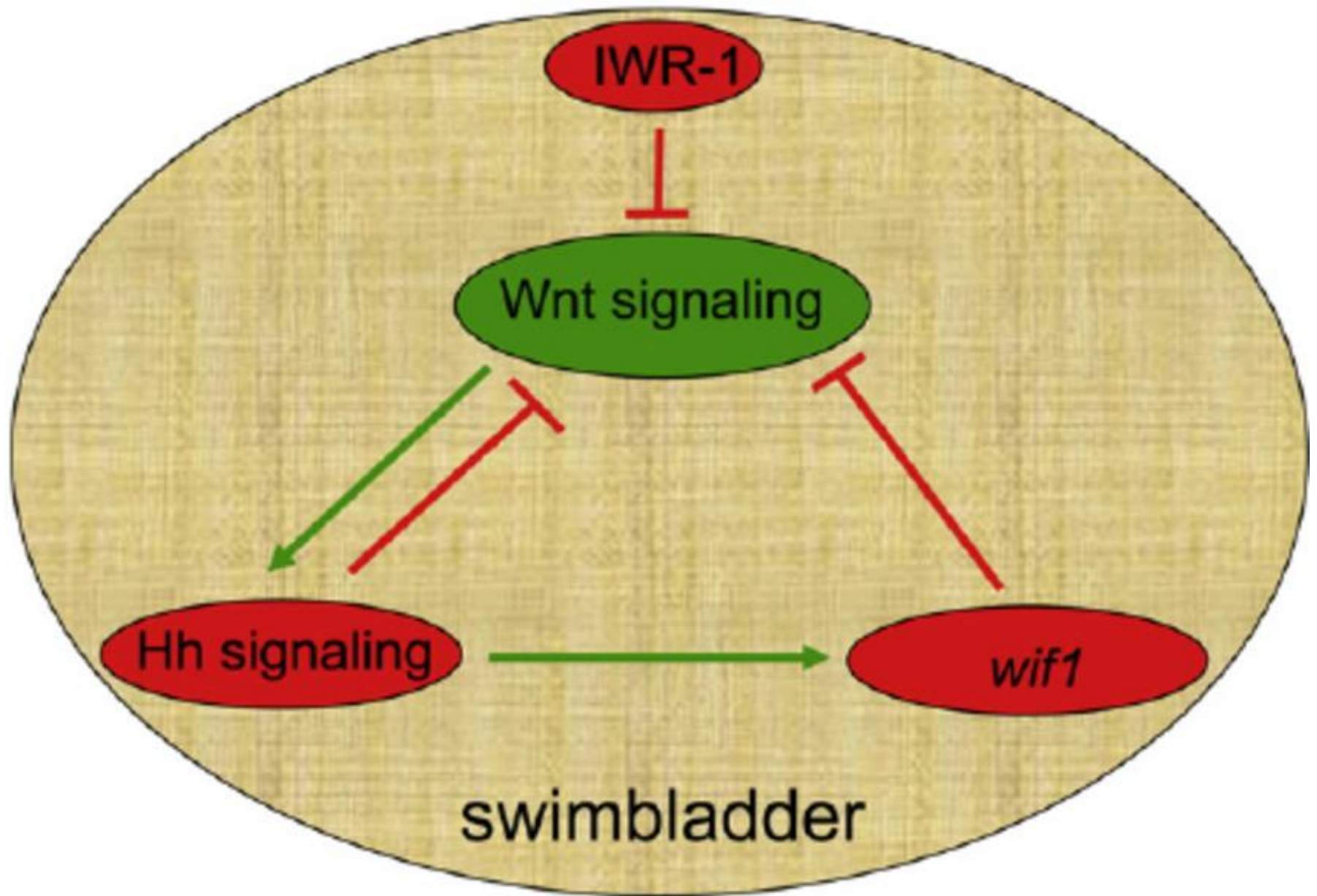
DNA Hypomethylation ➡ activate oncogenes

And initiate chromosome instability,

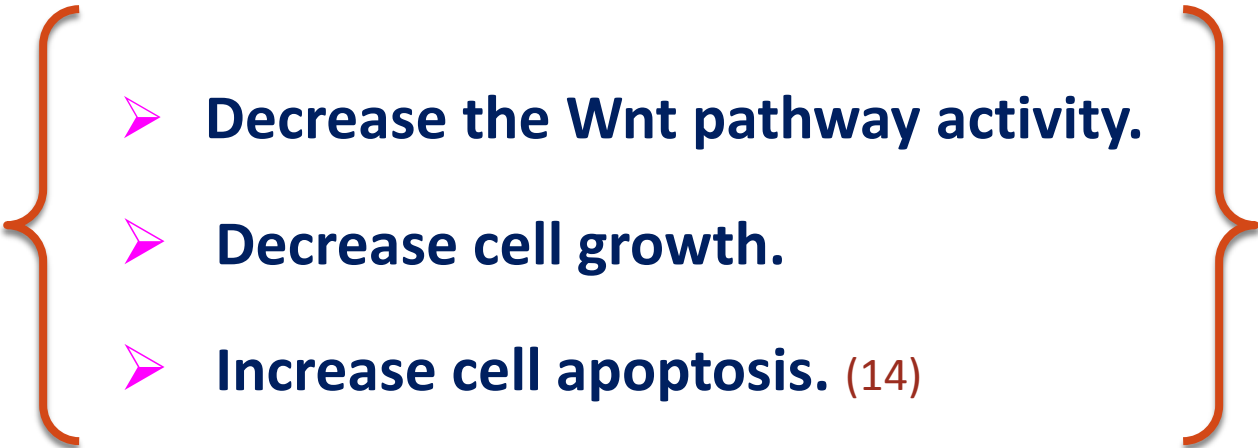
DNA Hypermethylation ➡ silencing of tumor suppressor genes.



DNA methylation is the addition of a methyl group (M) to the DNA base cytosine (C).



- ❖ *Wif1* antagonist of the Wnt pathway and is a **Tumor suppressor**.
(Epigenetic mechanisms in some tumors have been shown to cause inactivation of these genes.) (12)
- ❖ Tumor suppressor gene **hypermethylation CPG** areas in many cases have been reported in human cancer. (including colorectal cancer) . (13)

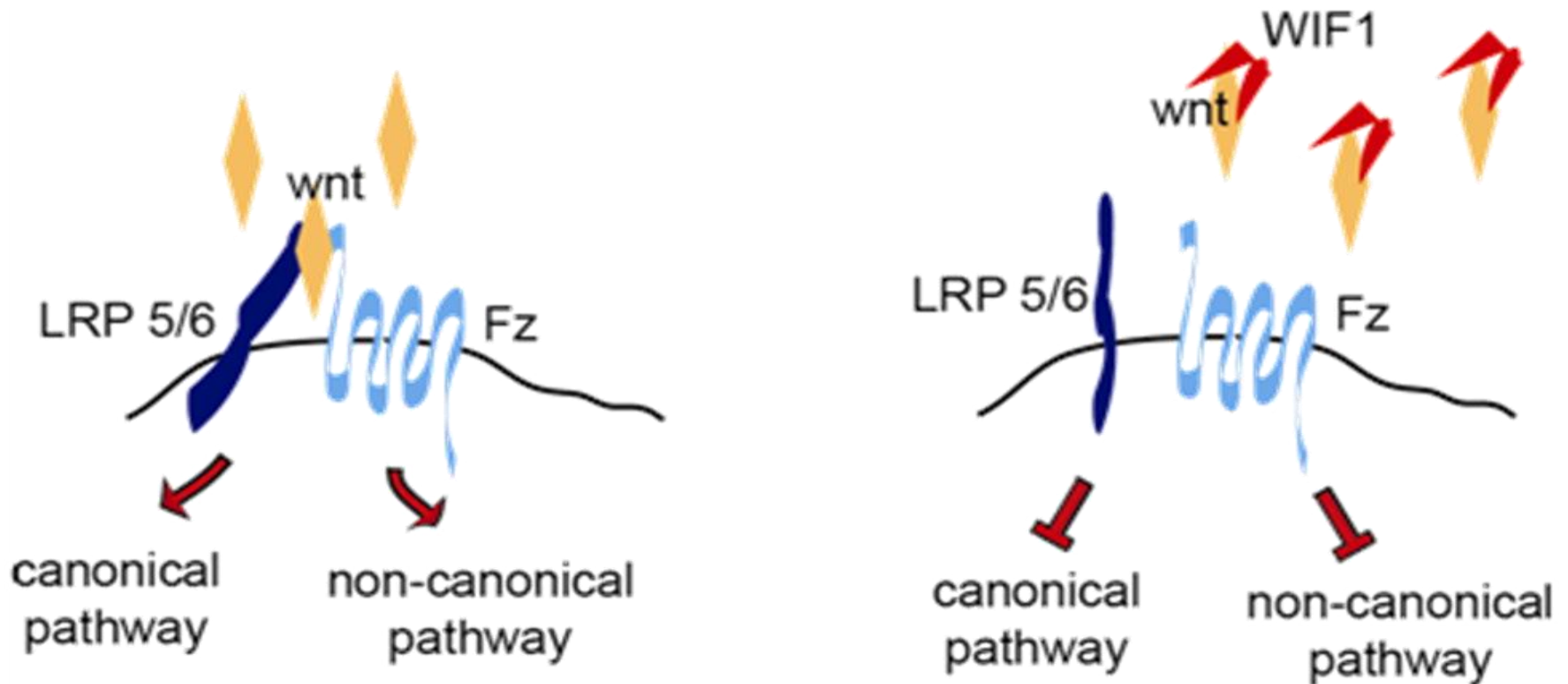
- 
- **Decrease the Wnt pathway activity.**
 - **Decrease cell growth.**
 - **Increase cell apoptosis.** (14)

wif1



- ✓ is targeted for epigenetic silencing in human breast cancer. (15)
- ✓ ***Wif1*** methylation is a prognostic marker for cancer of the mouth. (16)

- **Wif1** gene in cancers of the prostate and breast, lung and bladder was down regulated. (9)



❑ Jaroslaw.et all ; 2015

Analyze methylation of *Wif1* in 16 OSCC cell line and 43 tumor section from primary OC patient, frequently methylation was shown.

(9)

❑ Shanghui.et all ; 2015

Analyzed *Wif1*-expression level by IHC staining and semi-quantitative RT-PCR was shown, Wif1 in normal oral mucous tissue was expressed, and in OSCC with progression of disease, expression has been decreased. (17)

❑ Ramachandran et al., 2011:

WIF1 is downregulated by promoter **hypermethylation** in 87.5% of primary **cervical cancer**. (18)

❑ Lambiv et al., 2011:

WIF1 re-expression abolishes tumorigenicity of *glioblastoma cell lines* potentially by **inducing senescence**. (19)

❑ Rubin et al., 2010:

Hypermethylation of the **WIF1** promoter is found in the majority of osteosarcoma cell lines tested and it correlates with **WIF1 mRNA down regulation**. (20)

❑ Deng et al., 2010:

WIF1 is frequently **down regulated** through promoter **hypermethylation** in **HCC** . (21)

❑ Kawakami et al., 2009:

WIF1 is downregulated by promoter **hypermethylation** and when re-expressed **induces apoptosis** in *Renal cell carcinoma (RCC)* cells. (22)

❖ **Bladder cancer**

(Tang et al., 2009. 23)

❖ **Breast cancer**

(Ai et al., 2006. 24)

❖ **Gastrointestinal cancers**

(Taniguchi et al., 2005. 25)

✓ **Reduction in regulatory** of **WIF1** examined in many malignant tumors such as:

- ❑ Hepatocellular carcinoma Cancers . (26)
- ❑ Nasopharynx carcinoma Cancers . (27)
- ❑ Lung cancer. (28)
- ❑ Clone Cancers. (29)
- ❑ Esophageal adenocarcinoma Cancers . (30)
- ❑ Melanoma Cancers. (31)
- ❑ Bladder Cancers . (32)

- ✓ Decreased **WIF1** expression , correlated with methylation of CpG dinucleotides within the **WIF1** promoter. (33)
- ✓ Hypermethylation of **WIF1** gene promoter and low expression, activate Wnt signaling aberrantly and **induce** the development of **various human tumors**. (34)

WT₁

Normal biological functions

**Development of
genitourinary system**

Development of kidney

Adult kidney

Heart development

Neuron development

- The Wilms' tumor 1 (WT1) gene encodes a transcription factor important for normal cellular development and **cell survival**. (35)
- WT1 was initially discovered as a tumor suppressor in Wilms' tumor
- The N terminus of WT1 is negatively charged and contains a high concentration of prolin and glutamine residues. (36)

WT₁

❑ Laux DE. et al ;1999



detected aberrantly methylated sites in the **first intron** of the **WT₁** gene in **breast cancer**. (37)

❑ David M. et al ; 2001:

WT₁ is **overexpressed** in the majority of *primary breast tumors*. Tumor-specific methylation of the CpG island occurs in breast cancer but appears to be inconsequential to gene expression. (38)

❑ Oji Y.et all; 2003

In analyzed of **HNSCC** showed that **WT1** was not methylated. (39)

❑ Oji Y.et all ;2004

Overexpression of the **WT1** Gene in Esophageal Cancer. (40)

❑ Kaneuchi M.et all ;2005

examined The **WT1** promoter was significantly **methylated** in clear cell **adenocarcinoma** (88.2%) compared with serous adenocarcinoma (24.0%). (41)

❑ Moriya S. et al; 2008

Showed that , in **lung SCC** , **WT1** expression was **down regulated**. (42)

❑ Pierdonato B. et al., 2012

Hypermethylation of **WT1** gene could be involved in the carcinogenesis of **NSCLC** (non small cell lung cancer).

❑ Jitesh PV. et al; 2013

WT1 gene in **ESCC** and **Non ESCC** patient has different methylation status.

And show that, epigenetic changes Necessary for cancer development. (43)

❑ MikamiyT.et all; 2013

In analyze of **6 cell line of OSCC** with IHC , **WT1** was **over expressed**.
(44)

❑ Shimodaria S.et all; 2016

WT1 over expression was observed in autopsy sample of **pancreatic adenocarcinoma**. (45)

❑ Oji Y.et all; 2016

In leukemia **WT1** have high expression. (46)

offer

- Methylation of genes as biomarkers for cancer detection model can be used.
- Furthermore, by recognizing the methylation patterns in cancer types, it can also be used for treatment.



I thank
you!



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